

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

VirtualBox

RRID:SCR_011876

Type: Tool

Proper Citation

VirtualBox (RRID:SCR_011876)

Resource Information

URL: <https://www.virtualbox.org/>

Proper Citation: VirtualBox (RRID:SCR_011876)

Description: A general-purpose full virtualizer for x86 and AMD64/Intel64 hardware, targeted at server, desktop and embedded use.

Abbreviations: VirtualBox

Resource Type: software resource

Availability: GNU General Public License, v2

Resource Name: VirtualBox

Resource ID: SCR_011876

Alternate IDs: OMICS_01208

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260815T182436+0000

Ratings and Alerts

No rating or validation information has been found for VirtualBox.

No alerts have been found for VirtualBox.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 99 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Liu Z, et al. (2026) Metagenomic analysis of the DNA virome communities in swine lungs. *Frontiers in microbiology*, 17, 1798033.

Gkarane V, et al. (2026) Towards real-time pork breed and boar taint classification using rapid evaporative ionisation mass spectrometry. *NPJ science of food*, 10(1), 37.

Hriez S, et al. (2026) Measuring the impact of virtualization and containerization on the environment when using GPUs for processing the AI models. *Frontiers in big data*, 9, 1838191.

Settelmeier J, et al. (2025) MultiOmicsAgent: Guided Extreme Gradient-Boosted Decision Trees-Based Approaches for Biomarker-Candidate Discovery in Multiomics Data. *Journal of proteome research*, 24(6), 2816.

Block KT, et al. (2025) MRI4ALL: A Week-Long Hackathon for the Development of an Open-Source Ultra-Low-Field MRI System. *Journal of magnetic resonance imaging : JMRI*, 62(4), 959.

Lu X, et al. (2024) Metagenomic analysis reveals high diversity of gut viromes in yaks (*Bos grunniens*) from the Qinghai-Tibet Plateau. *Communications biology*, 7(1), 1097.

Lee JY, et al. (2024) Multi-omics analysis sandbox toolkit for swift derivations of clinically relevant genesets and biomarkers. *BMB reports*, 57(12), 521.

Zhang H, et al. (2024) ProcGCN: detecting malicious process in memory based on DGCNN. *PeerJ. Computer science*, 10, e2193.

Lötsch J, et al. (2024) Machine learning and biological validation identify sphingolipids as potential mediators of paclitaxel-induced neuropathy in cancer patients. *eLife*, 13.

Bashour H, et al. (2024) Biophysical cartography of the native and human-engineered antibody landscapes quantifies the plasticity of antibody developability. *Communications biology*, 7(1), 922.

Rischke S, et al. (2023) Machine learning identifies right index finger tenderness as key signal of DAS28-CRP based psoriatic arthritis activity. *Scientific reports*, 13(1), 22710.

Tsebriy O, et al. (2023) Machine learning-based phenotypic imaging to characterise the targetable biology of *Plasmodium falciparum* male gametocytes for the development of transmission-blocking antimalarials. *PLoS pathogens*, 19(10), e1011711.

Chouliaras N, et al. (2023) A novel autonomous container-based platform for cybersecurity training and research. *PeerJ. Computer science*, 9, e1574.

Ilca LF, et al. (2023) Enhancing Cyber-Resilience for Small and Medium-Sized Organizations with Prescriptive Malware Analysis, Detection and Response. *Sensors*

(Basel, Switzerland), 23(15).

Djaffardjy M, et al. (2023) Developing and reusing bioinformatics data analysis pipelines using scientific workflow systems. Computational and structural biotechnology journal, 21, 2075.

Mahmud I, et al. (2022) Performance Evaluation of MPTCP on Simultaneous Use of 5G and 4G Networks. Sensors (Basel, Switzerland), 22(19).

Huang M, et al. (2022) Spatiotemporal dynamics and functional characteristics of the composition of the main fungal taxa in the root microhabitat of *Calanthe sieboldii* (Orchidaceae). BMC plant biology, 22(1), 556.

Xu Y, et al. (2022) Validating the knowledge bank approach for personalized prediction of survival in acute myeloid leukemia: a reproducibility study. Human genetics, 141(9), 1467.

Johansen B, et al. (2022) First Evidence of a Combination of Terpinen-4-ol and ?-Terpineol as a Promising Tool against ESKAPE Pathogens. Molecules (Basel, Switzerland), 27(21).

Antunes AM, et al. (2022) A Pipeline for the Development of Microsatellite Markers using Next Generation Sequencing Data. Current genomics, 23(3), 175.